

Figure 1: 1/2

Sequence of the *Archaeoglobus fulgidus* exonuclease III gene:

SEQ ID NO.: 20/21

NO.: 20/21

ATGCTCAAAATCGCCACCTTCAACGTAACCTCCATCAGGAGCAGACTGCACATCGTGATT
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
TACGAGTTTTAGCGGTGGAAGTTGCATTTGAGGTAGTCCTCGTCTGACGTGTAGCACTAA
M L K I A T F N V N S I R S R L H I V I -
CCGTGGCTGAAGGAGAACAAGCCTGACATTCTATGCATGCAGGAGACGAAGGTTGAGAAC
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
GGCACCGACTTCCTCTTGTTTCGGACTGTAAGATACGTACGTCCTCTGCTTCCAACCTCTG
P W L K E N K P D I L C M Q E T K V E N -
AGGAAGTTTCCTGAGGCCGATTTTCACCGCATCGGCTACCACGTCGTCTTCAGCGGGAGC
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
TCCTTCAAAGGACTCCGGCTAAAAGTGGCGTAGCCGATGGTGCAGCAGAAGTCGCCCTCG
R K F P E A D F H R I G Y H V V F S G S -
AAGGGAAGGAATGGAGTGGCCATAGCTTCCCTCGAAGAGCCTGAGGATGTCAGCTTCGGT
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
TTCCCTTCCTTACCTCACCGGTATCGAAGGGAGCTTCTCGGACTCCTACAGTCGAAGCCA
K G R N G V A I A S L E E P E D V S F G -
CTCGATTGAGAGCCGAAGGACGAGGACAGGCTGATAAGGGCAAAGATAGCTGGCATAGAC
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
GAGCTAAGTCTCGGCTTCCTGCTCCTGTCCGACTATCCCGTTTCTATCGACCGTATCTG
L D S E P K D E D R L I R A K I A G I D -
GTGATTAACACCTACGTTCTCAGGGATTCAAAATTGACAGCGAGAAGTACCAGTACAAG
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
CACTAATTGTGGATGCAAGGAGTCCCTAAGTTTTAACTGTCGCTCTTCATGGTCATGTTT
V I N T Y V P Q G F K I D S E K Y Q Y K -
CTCCAGTGGCTTGAGAGGCTTTACCATTACCTTCAAAAAACCGTTGACTTCAGAAGCTTT
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
GAGGTCACCGAACTCTCCGAAATGGTAATGGAAGTTTTTTGGCAACTGAAGTCTTCGAAA
L Q W L E R L Y H Y L Q K T V D F R S F -
GCTGTTTGGTGTGGAGACATGAACGTTGCTCCTGAGCCAATCGACGTTCACTCCCCAGAC
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
CGACAAACCACACCTCTGTACTTGCAACGAGGACTCGGTTAGCTGCAAGTGAGGGGTCTG
A V W C G D M N V A P E P I D V H S P D -
AAGCTGAAGAACCACGTCTGCTTCCACGAGGATGCGAGAAGGGCATACAAAAAATACTC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
TTCGACTTCTTGGTGCAGACGAAGGTGCTCCTACGCTCTTCCCGTATGTTTTTTTATGAG
K L K N H V C F H E D A R R A Y K K I L -

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GAACTCGGCTTTGTTGACGTGCTGAGAAAAATACATCCCAACGAGAGAATTTACACCTTC
541 -----+-----+-----+-----+-----+ 600
CTTGAGCCGAAACAACCTGCACGACTCTTTTATGTAGGGTTGCTCTCTTAAATGTGGAAG
a E L G F V D V L R K I H P N E R I Y T F -
TACGACTACAGGGTTAAGGGAGCCATTGAGCGGGGGCTGGGATGGAGGGTTGATGCCATC
601 -----+-----+-----+-----+-----+ 660
ATGCTGATGTCCCAATTCCCTCGGTAACCTCGCCCCGACCCTACCTCCCAACTACGGTAG
a Y D Y R V K G A I E R G L G W R V D A I -
CTCGCCACCCACCCCTCGCCGAAAGATGCGTGGAAGTGTACGCAGACATCAAACCGAGG
661 -----+-----+-----+-----+-----+ 720
GAGCGGTGGGGTGGGGAGCGGCTTTCTACGCACCTGACGATGCGTCTGTAGTTTGGCTCC
a L A T P P L A E R C V D C Y A D I K P R -
CTGGCAGAAAAGCCATCCGACCACCTCCCTCTCGTTGCTGTGTTTGACGTGTAG
721 -----+-----+-----+-----+-----+ 774
GACCGTCTTTTCGGTAGGCTGGTGGAGGGAGAGCAACGACACAACTGCACATC
a L A E K P S D H L P L V A V F D V * -

Figure 2:

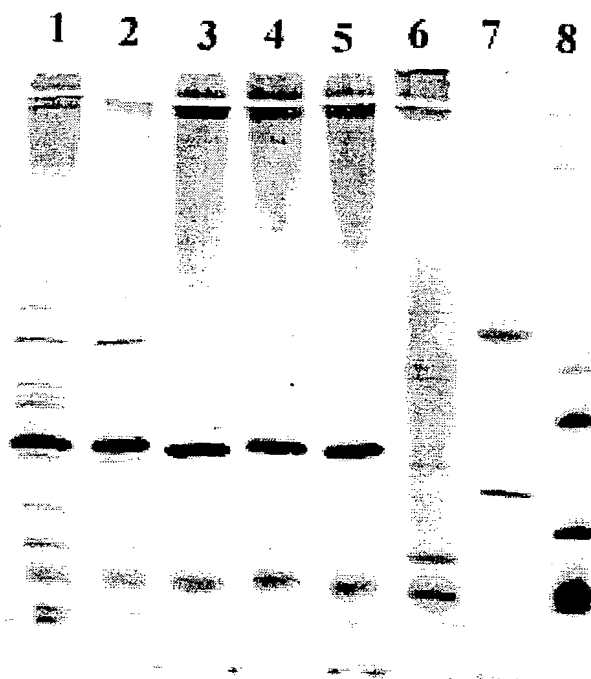
Temperature stability of *Afu* exonuclease III

Figure 3:

Test for exonuclease III activity

1 2 3 4 5 6 7 8 9 10 11 12 13 14

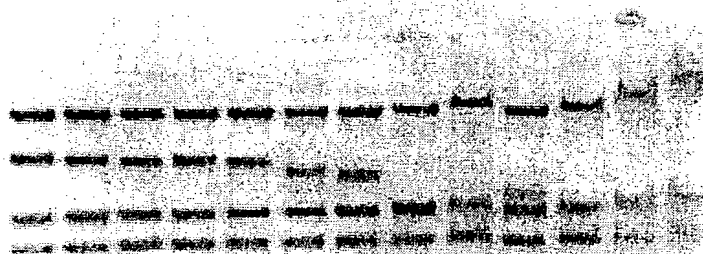


Figure 4:

Principle of the 3'-primer correction assay

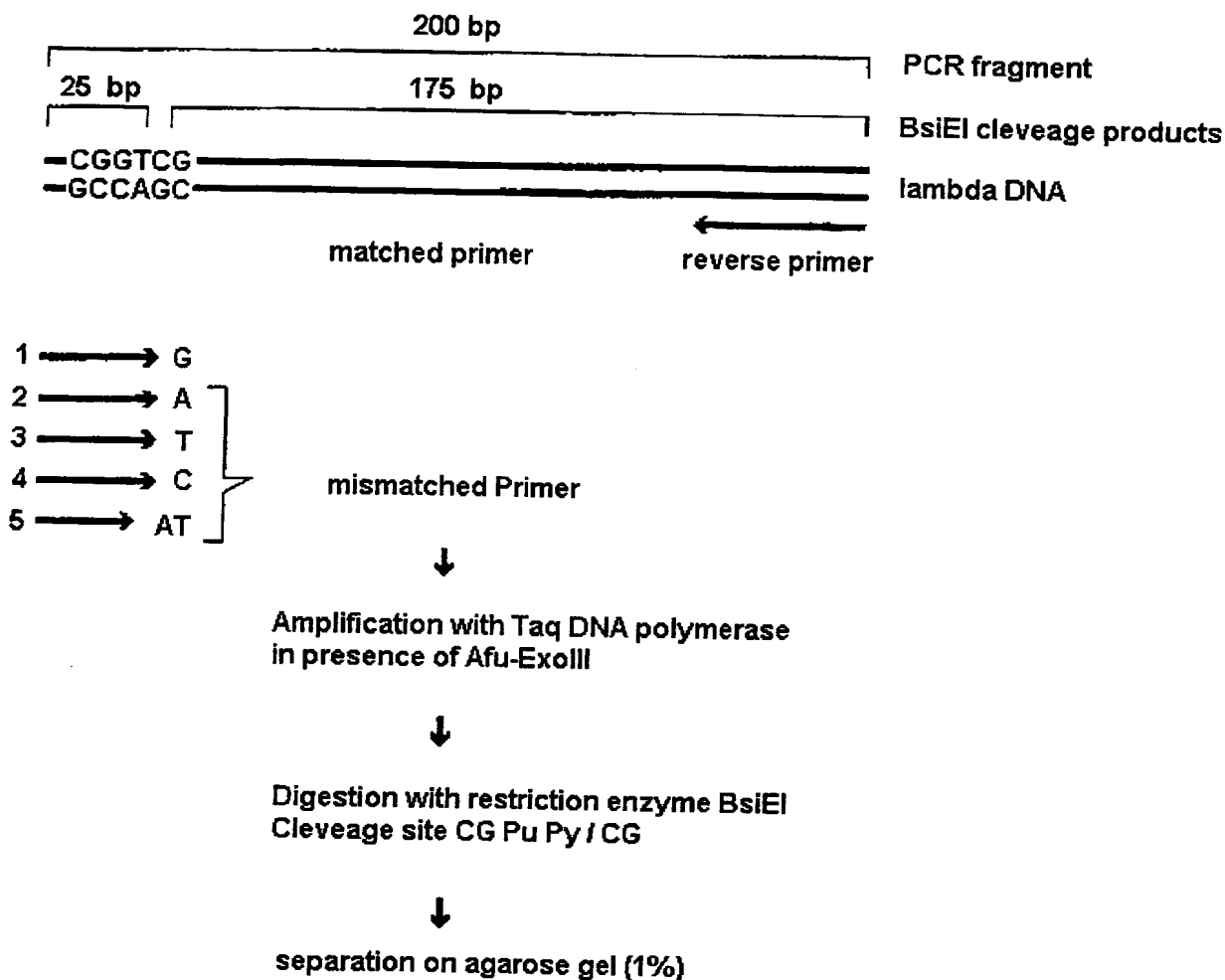
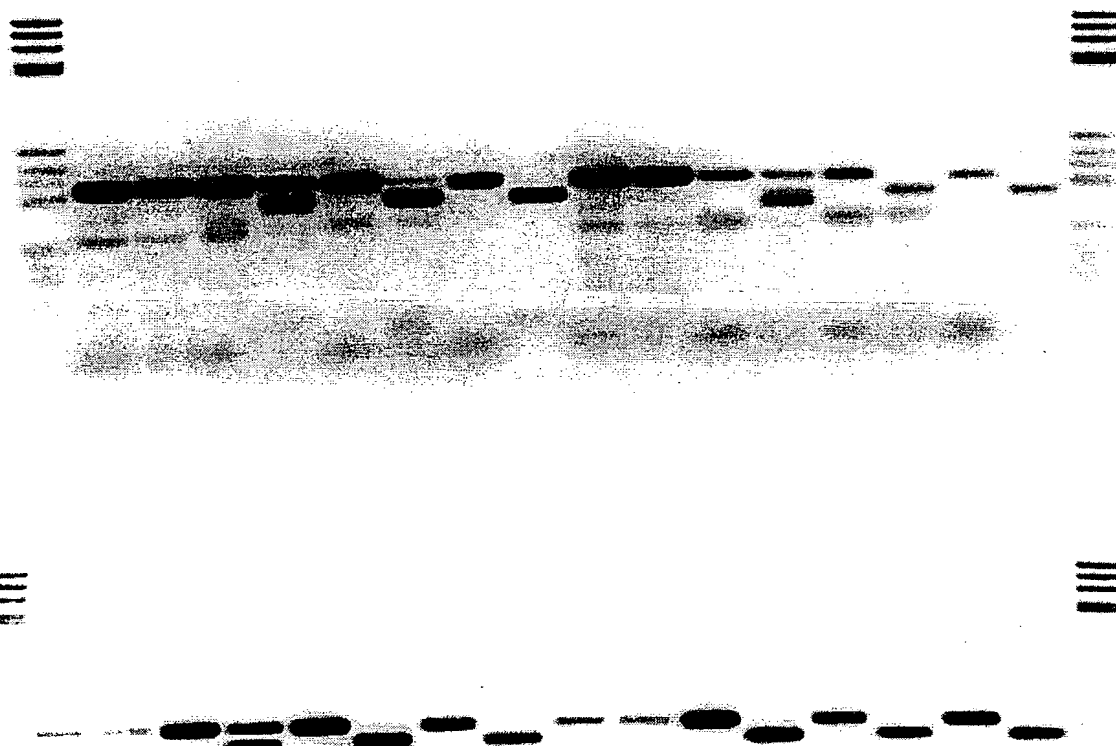


Figure 5:

Mismatched primer correction in PCR

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18



19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

Figure 6A

Error rates of different DNA polymerases in PCR

Polymerase	Template conc. (ng)	yield (ng)	DNA duplica- tions d	blue colonies lacI ⁻	white colonies lac ⁺	total number of colonies	% lac ⁺	error rate (f ₃₄₉)
Taq Ch.	10	11650	10.2	130	2261	2391	5.4	1.57 x 10 ⁻³
HiFi Ch.	10	11550	10.2	40	5458	5498	0.72	2.06 x 10 ⁻⁶
Pwo	10	9675	9.9	17	5891	5908	0.29	8.32 x 10 ⁻⁷
Taq/Exo 1	10	11550	10.2	94	4291	4385	2.14	6.10 x 10 ⁻⁵
Taq/Exo 2	10	11125	10.1	146	7644	7790	1.87	5.36 x 10 ⁻⁵
Taq/Exo 3	10	8500	9.7	133	8188	8321	1.6	4.74 x 10 ⁻⁵
Taq/Exo 4	10	1292	7	79	7236	7315	1.08	4.44 x 10 ⁻⁵
Taq/Exo 5	10	236	4.6	25	2674	2724	0.92	1.16 x 10 ⁻⁵

* Due to the unfavorable ratio of Taq:Exo the product yield was low. This results in an apparently low amplification efficiency d, which is an important parameter in the formula used for the calculation of the error rate.

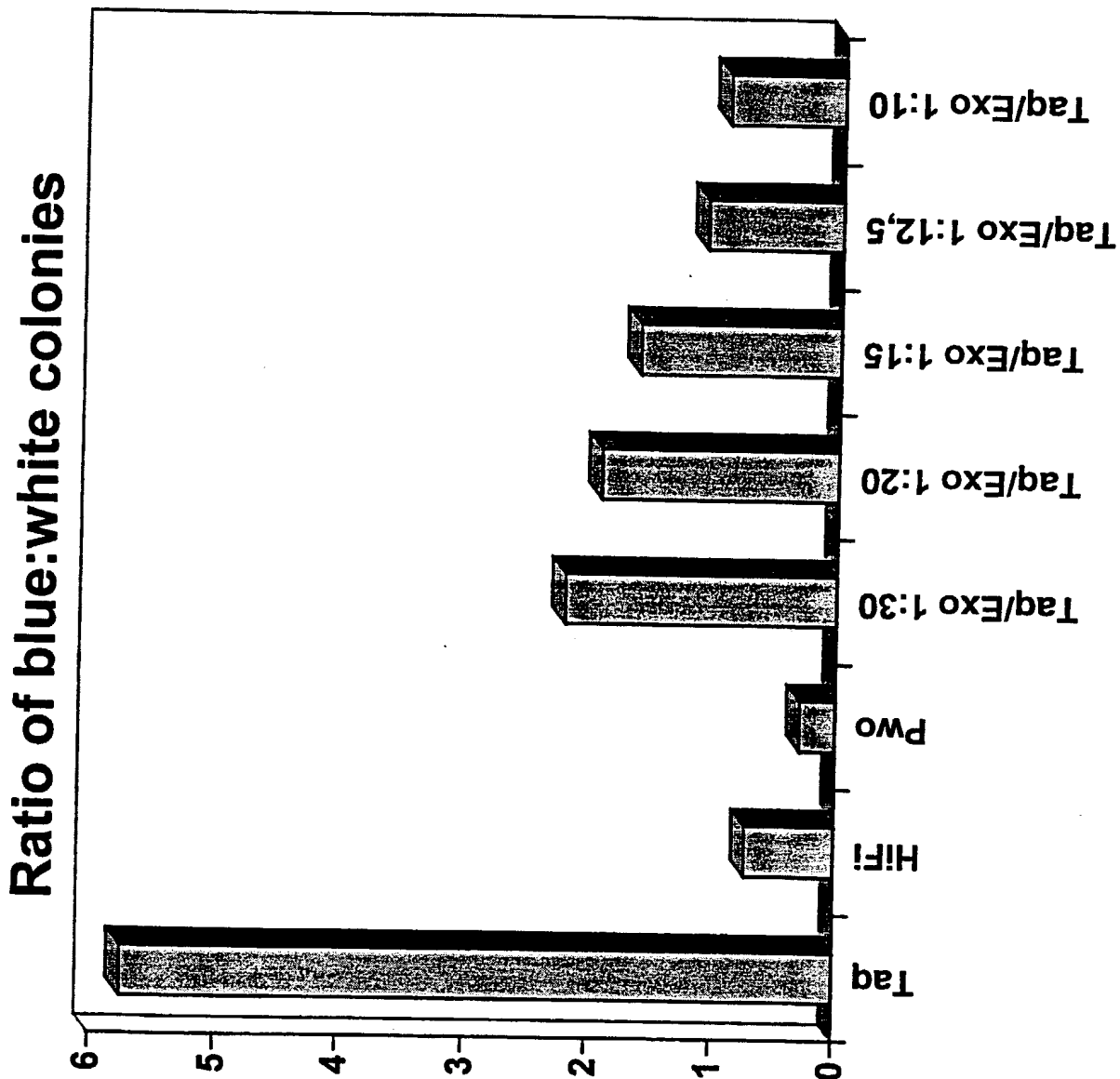
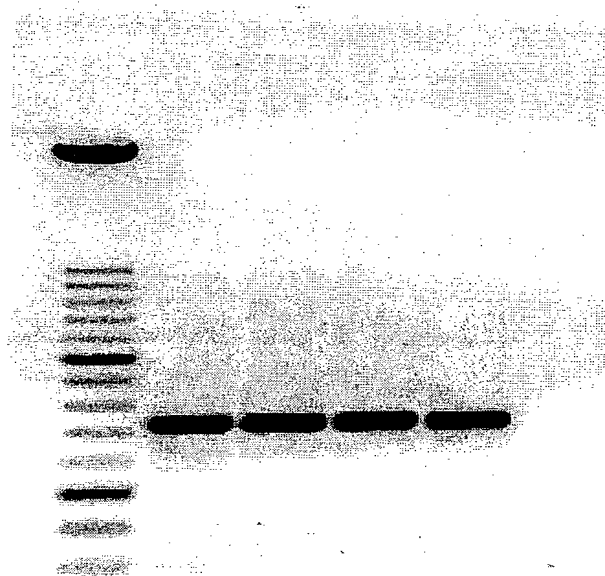


Figure 6B:

Figure 7:

1 2 3 4 5 6



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Figure 8:

UNG treatment of dUMP containing PCR products

1 2 3 4 5 6 7 8 9

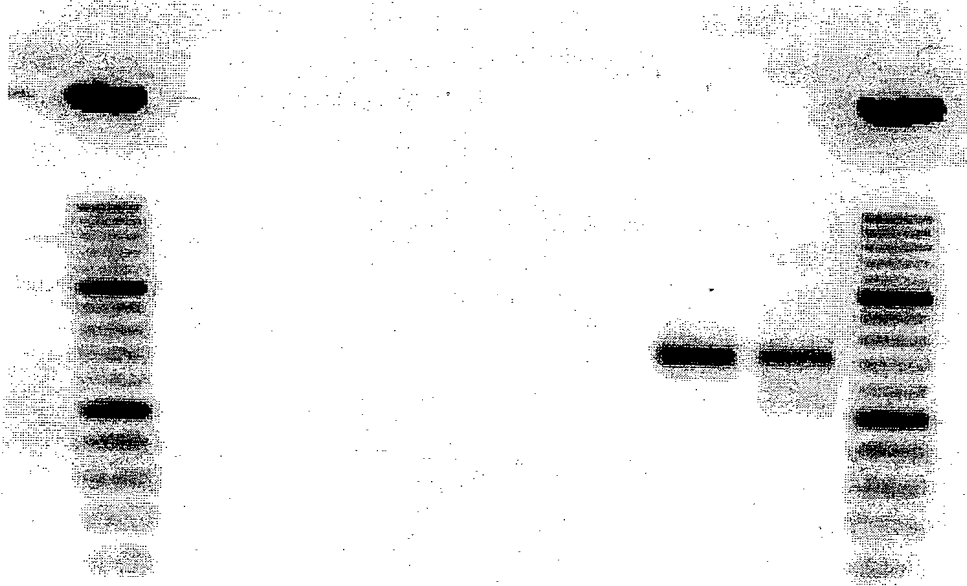


Figure 9:

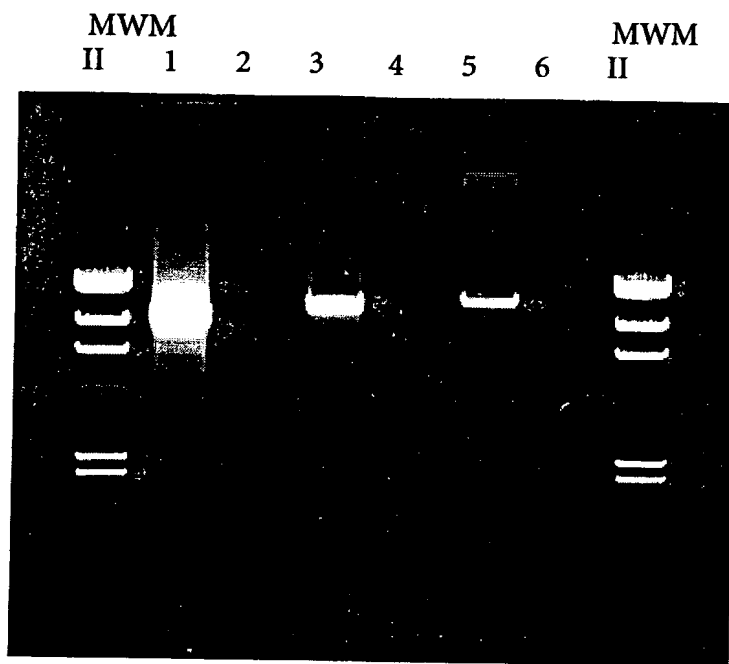


Figure 10:

1	2	3	4	5	6	7	8	9	10
MWM	1	2	3	4	5	6	7	8	MWM

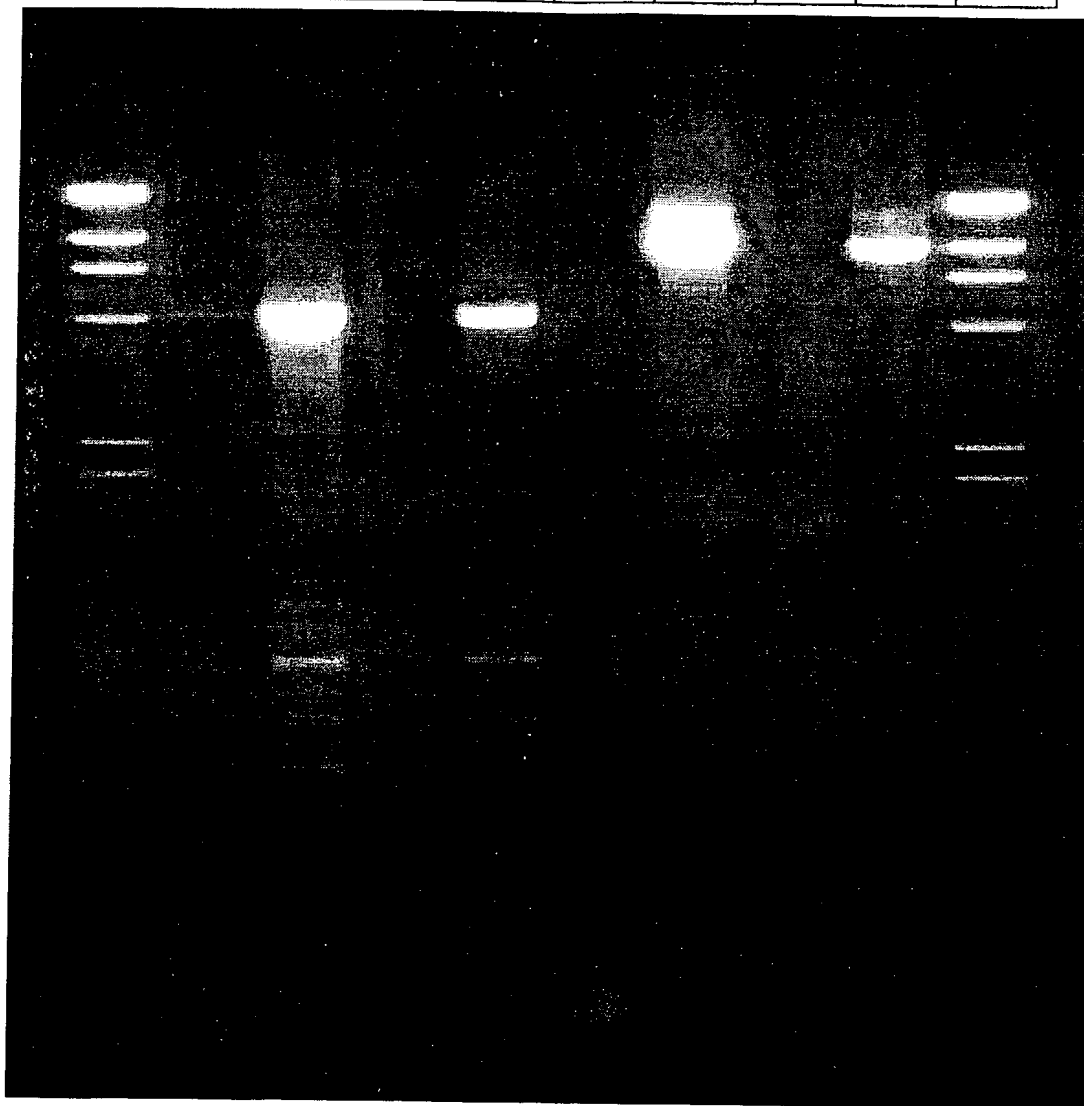


Figure 11

1	2	3	4	5	6	7	8	9
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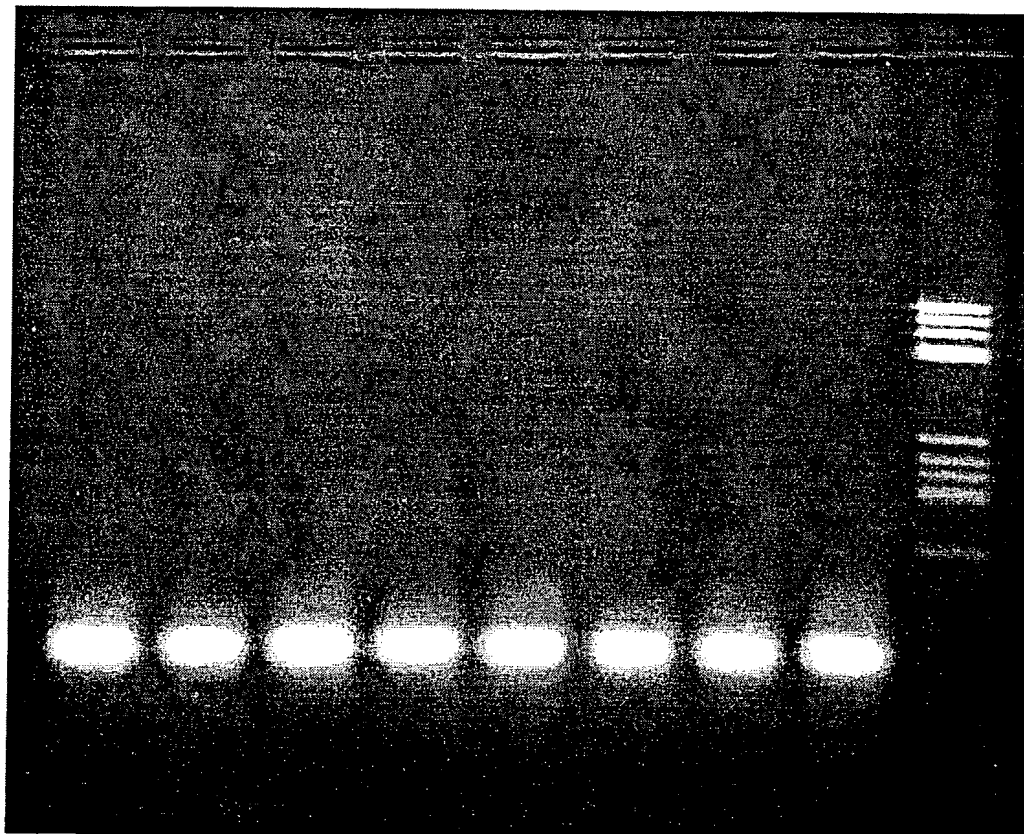


Figure 12

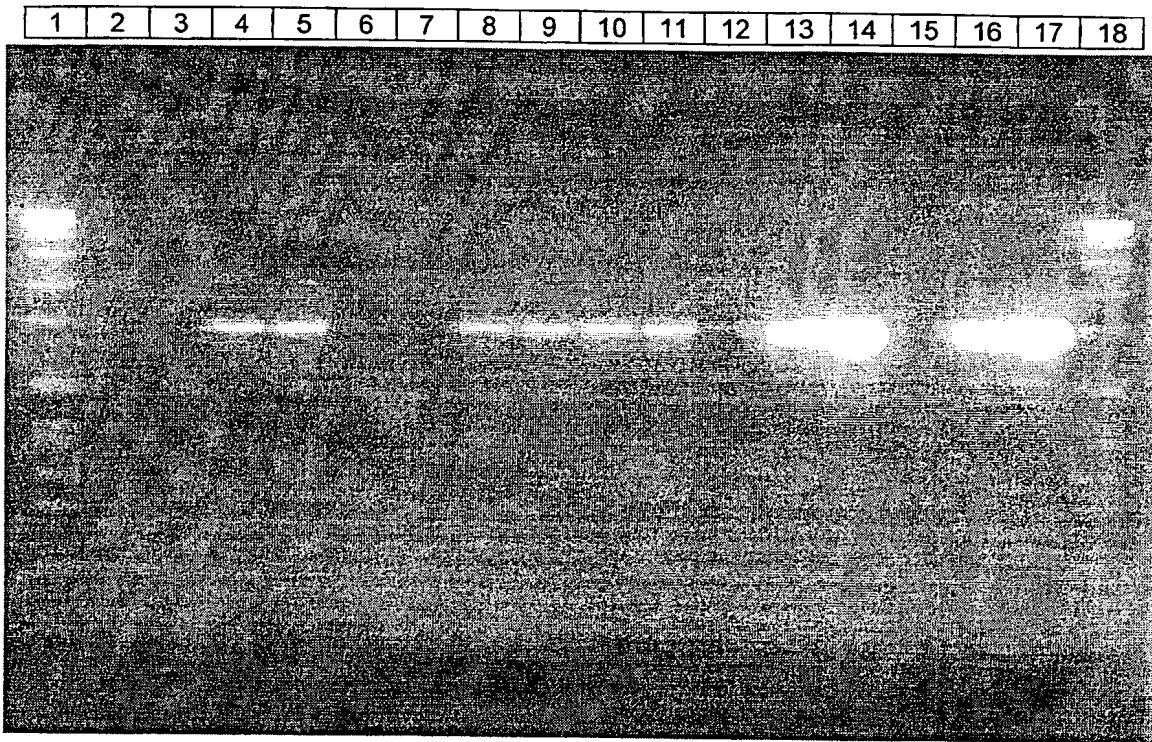


Figure 12